120 Duplication in *CHIT1* gene and the risk for *Aspergillus* lung disease in CF patients

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Background: *Aspergillus* often persists in the respiratory tract of patients with Cystic Fibrosis (CF) and may cause allergic broncho pulmonary aspergillosis (ABPA). Chitinases are enzymes that digest the chitin polymer. Plants use chitinase as a defense mechanism against fungi. Chitotriosidase (*CHIT1*) is the major chitinase in human airways. Variation in the coding region with 24-bp duplication allele results in reduced *CHIT1* activity. Recently, *CHIT1* duplication heterozygocity was found in 6/6 patients with severe asthma and fungal sensitization (SAFS).
Our aim was to evaluate the link between *CHIT1* duplication in CF patients and the predisposition to Allergic bronchopulmonary mycosis (ABPM) or persistent *Aspergillus* positive sputum (APS).
Patients and Methods: *CHIT1* duplication was assessed in three CF groups.
Group 1: patients who had neither ABPA nor APS in the past (control group).
Group 2: patients with persistent APS (⩾2/year), without ABPA.
Group 3: patients with current or past ABPM.
Results: Forty patients with CF were included in the analysis, *CHIT1* duplication heterozygocity was found in 3/6 (50%) of the patients in the ABPM group, 3/12 (25%) in the APS group, and 7/22 (31.8%) in the control group ($P > 0.05$). Eleven patients were heterozygous for W1282X CF mutation, 90.9% were negative for *CHIT1* duplication. Five patients were homozygous for W1282X; none of them had *CHIT1* duplication or ABPA.
Conclusions: *CHIT1* duplication is not found in all CF patients with ABPM in contrast to patients with SAFS. These results suggest that *CHIT1* duplication cannot be the sole explanation for fungal positive sputum in CF patients.

121 *Candida* colonisation status in adults and children with cystic fibrosis

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Objectives: Previously believed to be an innocent bystander in the cystic fibrosis (CF) microbiome, *Candida* has recently been considered to be a potential pathogen in the CF airway. *Candida* colonisation has been shown to predict a greater FEV_1 decline, and to also increase the rate of exacerbations in people with CF [1].
Methods: Here we characterised the *Candida* colonisation status of people with CF attending three hospitals in Dublin. Sputum was spontaneously expectorated from a deep cough and bronchoalveolar lavage (BAL) was obtained via fibre-optic bronchoscopy. Samples were liquefied and serially diluted before plating on CHROMagar and incubating at 37ºC for 48 hours. Based on the hydrolysis of hexosaminidase in the media, *Candida* isolates were differentiated by colour. *C. dubliniensis* is indistinguishable from *C. albicans* on this agar, however subculture and further incubation at 45ºC inhibits growth of *C. dubliniensis*. Of 80 sputum samples from 44 adults with CF (30 male, 14 female; average age 25.8 years ±8.8), 63% of the adults (n = 28) were positive for *Candida* in at least one of their sputum samples. 59% (n = 26), 13% (n = 6) and 4% (n = 2) had *C. albicans*, *C. krusei* and *C. dubliniensis* respectively. BAL samples from 11 children with CF (4 male, 7 female; average age 3.4±2.1 years) were also cultured; none were positive for *Candida*.
Conclusion: *C. albicans* is the most common *Candida* isolate in the sputum of adults with CF. *Candida* was not present in pediatric BAL samples, indicating that it may only be acquired at later stages, possibly after prolonged exposure to broad-spectrum antibiotics.

Reference(s)

[1] Chotirmall SH et al. Chest. 2011; 5: 1186–1195.

122 The impact of human rhinovirus infection on the cystic fibrosis lung microbiome

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Objectives: Human rhinovirus is the most common viral respiratory infection amongst patients with CF and is associated with significant morbidity. The effect of rhinovirus infection on the CF lung microbiome is unknown.
Methods: 5 adult CF patients with acute rhinovirus infection were identified. Sequential respiratory tract samples were collected during clinical stability, rhinovirus infection and recovery. Standard bacterial culture and 16S rRNA pyrosequencing were performed on paired sputum samples at each visit. A PCR panel for 9 respiratory viruses was also performed on sputum, nose- & throat-swabs. The Shannon Index was calculated to quantify sputum bacterial diversity and analysed using generalised estimating equation models.
Results: Median age of the patients was 31 years and all took regular azithromycin and a nebulized antibiotic. 4/5 patients commenced additional antibiotics at the time of rhinovirus infection. 16S rRNA pyrosequencing showed that rhinovirus infection was associated with a substantial change in bacterial diversity in 4/5 patients. The mean (SD) Shannon Index increased from 0.33 (0.46) at baseline to 0.74 (0.41) at the virus-positive visit ($p = 0.1$). The mean Shannon Index fell to 0.19 (0.08) at recovery ($p < 0.001$). In 3/5 cases rhinovirus was associated with a large increase in the proportion of *Streptococcus* spp. and a corresponding decrease in the proportion of the previously predominant bacterial pathogen.
Conclusion: Rhinovirus infection is frequently associated with changes in the bacterial diversity of CF sputum. The interaction between rhinovirus and *Streptococcus* spp. in CF pulmonary exacerbations requires further exploration.